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RAW SEQUENCE LISTING

DATE: 07/20/2001

PATENT APPLICATION: US/09/822,698A

TIME: 13:28:54

Input Set : A:\SEQ DYX-015.1.txt

Output Set: N:\CRF3\07202001\I822698A.raw

3 <110> APPLICANT: Hoogenboom, Hendricus R.J.M.
 4 Henderikx, Maria P.G.
 6 <120> TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
 8 <130> FILE REFERENCE: DYX-015.1 US
 10 <140> CURRENT APPLICATION NUMBER: 09/822,698A
 11 <141> CURRENT FILING DATE: 2001-03-30
 13 <150> PRIOR APPLICATION NUMBER: US 09/538,913
 14 <151> PRIOR FILING DATE: 2000-03-30
 16 <160> NUMBER OF SEQ ID NOS: 112
 18 <170> SOFTWARE: Microsoft Word
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 113
 22 <212> TYPE: PRT
 23 <213> ORGANISM: artificial sequence
 25 <220> FEATURE:
 26 <223> OTHER INFORMATION: light chain variable region of the MUC1-specific
 27 binding domain of PH1 Fab antibody
 29 <400> SEQUENCE: 1
 31 Glu Ile Val Leu Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
 32 1 5 10 15
 34 Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
 35 20 25 30
 37 Asn Gly Tyr Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 38 35 40 45
 40 Pro Gln Leu Leu Ile Tyr Ser Gly Ser His Arg Ala Ser Gly Val Pro
 41 50 55 60
 43 Asp Arg Phe Ser Gly Ser Val Ser Gly Thr Asp Phe Thr Leu Arg Ile
 44 65 70 75 80
 46 Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly
 47 85 90 95
 49 Leu Gln Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
 50 100 105 110
 52 Arg
 55 <210> SEQ ID NO: 2
 56 <211> LENGTH: 339
 57 <212> TYPE: DNA
 58 <213> ORGANISM: artificial sequence
 60 <220> FEATURE:
 61 <223> OTHER INFORMATION: nucleotide sequence coding for amino acid sequence of
 62 SEQ ID NO:1
 64 <400> SEQUENCE: 2
 66 gaaattgtgc tgactcagtc tccactctcc ctgcccgta cccctggaga gccggcctcc 60
 68 atctcctgca ggtctagtca gagcctcctg catagtaatg gatacaccta tttggattgg 120
 70 tacctgcaga agccagggca gtctccacag ctctgatct attcgggttc tcatcgggcc 180
 72 tccgggggtcc ctgacaggtt cagtggcagt gtatcaggca cagattttac actgagaatc 240
 74 agcagagtgg aggctgagga tgttgaggtt tattactgca tgcagggtct acagagtcca 300
 76 ttcactttcg gccctgggac caaagtggat atcaaacga 339

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See page 5

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79 <210> SEQ ID NO: 3
80 <211> LENGTH: 121
81 <212> TYPE: PRT
82 <213> ORGANISM: artificial sequence
84 <220> FEATURE:
85 <223> OTHER INFORMATION: heavy chain variable region of the MUC1-specific
86 binding domain of the PH1 Fab antibody
88 <400> SEQUENCE: 3
90 Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
91 1 5 10 15
93 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Asn
94 20 25 30
96 Ala Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
97 35 40 45
99 Ser Gly Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
100 50 55 60
102 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
103 65 70 75 80
105 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
106 85 90 95
108 Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asp Tyr Trp Gly
109 100 105 110
111 Gln Gly Thr Leu Val Thr Val Ser Ser
112 115 120
115 <210> SEQ ID NO: 4
116 <211> LENGTH: 363
117 <212> TYPE: DNA
118 <213> ORGANISM: artificial sequence
120 <220> FEATURE:
121 <223> OTHER INFORMATION: nucleotide sequence coding for amino acid sequence of
122 SEQ ID NO:3
124 <400> SEQUENCE: 4
126 caggtccagc tgggtgcagtc tgggggaggc ttggtacagc ctgggggggct cctgagactc 60
128 tcctgtgcag cctctggatt cacgtttaga agtaacgcca tgggctgggt ccgccaggct 120
130 ccagggaagg ggctggagtg ggtctcaggt attagtggta gtggtggcag cacatactac 180
132 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
134 ctgcaaatga acagcctgag agccgaggac acggccgtat attattgtgc gaaacatacc 300
136 ggggggggagc tttgggaccc cattgactac tggggccagg gaaccctggt caccgtctca 360
138 agc 363
141 <210> SEQ ID NO: 5
142 <211> LENGTH: 381
143 <212> TYPE: PRT
144 <213> ORGANISM: artificial sequence
146 <220> FEATURE:
147 <223> OTHER INFORMATION: MUC1-specific immunocytokine bivPH1-IL-2
149 <400> SEQUENCE: 5
151 Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
152 1 5 10 15
154 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Asn

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155          20          25          30
157 Ala Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
158          35          40          45
160 Ser Gly Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
161          50          55          60
163 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
164 65          70          75          80
166 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
167          85          90          95
169 Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asp Tyr Trp Gly
170          100         105         110
172 Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ala Leu Glu Ile
173          115         120         125
175 Val Leu Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly Glu Pro
176          130         135         140
178 Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly
179 145          150         155         160
181 Tyr Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln
182          165         170         175
184 Leu Leu Ile Tyr Ser Gly Ser His Arg Ala Ser Gly Val Pro Asp Arg
185          180         185         190
187 Phe Ser Gly Ser Val Ser Gly Thr Asp Phe Thr Leu Arg Ile Ser Arg
188          195         200         205
190 Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Leu Gln
191          210         215         220
193 Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Gly
194 225          230         235         240
196 Gly Gly Ser Gly Gly Gly Ala Leu Ala Pro Thr Ser Ser Ser Thr Lys
197          245         250         255
199 Lys Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile
200          260         265         270
202 Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu
203          275         280         285
205 Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu
206          290         295         300
208 Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu
209 305          310         315         320
211 Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn
212          325         330         335
214 Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met
215          340         345         350
217 Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg
218          355         360         365
220 Trp Ile Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr
221          370         375         380
224 <210> SEQ ID NO: 6
225 <211> LENGTH: 1143
226 <212> TYPE: DNA
227 <213> ORGANISM: artificial sequence

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229 <220> FEATURE:
230 <223> OTHER INFORMATION: nucleotide sequence coding for amino acid sequence of
231     SEQ ID NO:5
233 <400> SEQUENCE: 6
235 caggtccagc tgggtgcagtc tggggggaggc ttggtacagc ctgggggggct cctgagactc      60
237 tcctgtgcag cctctggatt cacgtttaga agtaacgccca tgggctgggt ccgccaggct      120
239 ccagggaagg ggctggagtg ggtctcaggt attagtggta gtggtggcag cacatactac      180
241 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa caccgtgtat      240
243 ctgcaaatac acagcctgag agccgaggac acggccgtat attattgtgc gaaacatacc      300
245 ggggggggcg tttgggaccc cattgactac tggggccagg gaaccctggt caccgtctca      360
247 agcggaggcg gtgcacttga aattgtgctg actcagtctc cactctccct gcccgtcacc      420
249 cctggagagc cggcctccat ctctgcagc tctagtcaga gcctcctgca tagtaatgga      480
251 tacacctatt tggattggta cctgcagaag ccagggcagt ctccacagct cctgatctat      540
253 tcgggttctc atcgggcctc cgggggtccct gacagggttca gtggcagtg atcaggcaca      600
255 gattttacac tgagaatcag cagagtggag gctgaggatg ttggagtta ttactgcatg      660
257 cagggtctac agagtccatt cactttcggc cctgggacca aagtggatat caaacgaggg      720
259 ggtggatcag gcggcggggc cctagcacct acttcaagtt ctacaaagaa aacacagcta      780
261 caactggagc atttactgct ggatttacag atgattttga atggaattaa taattacaag      840
263 aatcccaaac tcaccaggat gtcacattt aagttttaca tgcccaagaa ggccacagaa      900
265 ctgaaacatc ttcagtgtct agaagaagaa ctcaaacctc tggaggaagt gctaaattta      960
267 gctcaaagca aaaactttca cttaagaccc agggacttaa tcagcaatat caacgtaata     1020
269 gttctggaac taaagggatc tgaaacaaca ttcattgtgt aatatgctga tgagacagca     1080
271 accattgtag aatttctgaa cagatggatt accttttgtc aaagcatcat ctcaacactg     1140
273 act                                     1143
276 <210> SEQ ID NO: 7
277 <211> LENGTH: 20
278 <212> TYPE: PRT
279 <213> ORGANISM: artificial sequence
281 <220> FEATURE:
282 <223> OTHER INFORMATION: peptide of MUC1 protein
284 <400> SEQUENCE: 7
286 Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly
287 1           5           10           15
288 Ser Thr Ala Pro
289           20
292 <210> SEQ ID NO: 8
293 <211> LENGTH: 20
294 <212> TYPE: PRT
295 <213> ORGANISM: artificial sequence
297 <220> FEATURE:
298 <223> OTHER INFORMATION: peptide of MUC1 protein
300 <400> SEQUENCE: 8
302 Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro
303 1           5           10           15
305 Pro Ala His Gly
306           20
309 <210> SEQ ID NO: 9
310 <211> LENGTH: 24
311 <212> TYPE: DNA

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312 <213> ORGANISM: artificial sequence
314 <220> FEATURE:
315 <223> OTHER INFORMATION: CH1FOR primer
317 <400> SEQUENCE: 9
319 gtccttgacc aggcagccca gggc                24
322 <210> SEQ ID NO: 10
323 <211> LENGTH: 23
324 <212> TYPE: DNA
325 <213> ORGANISM: artificial sequence
327 <220> FEATURE:
328 <223> OTHER INFORMATION: pUC-reverse primer
330 <400> SEQUENCE: 10
332 agcggataac aatttcacac agg                23
335 <210> SEQ ID NO: 11
336 <211> LENGTH: 44
337 <212> TYPE: DNA
338 <213> ORGANISM: artificial sequence
340 <220> FEATURE:
341 <223> OTHER INFORMATION: VL backward primer
343 <400> SEQUENCE: 11
345 accgctcca ccagtgcact tgaaattgtg ctgactcagt ctcc    44
348 <210> SEQ ID NO: 12
349 <211> LENGTH: 51
350 <212> TYPE: DNA
351 <213> ORGANISM: artificial sequence
353 <220> FEATURE:
354 <223> OTHER INFORMATION: VL forward primer
356 <400> SEQUENCE: 12
358 accgctcca ccgggcgcgc cttattaaca ctctcccctg ttgaagctct t    51
361 <210> SEQ ID NO: 13
362 <211> LENGTH: 61
363 <212> TYPE: DNA
364 <213> ORGANISM: artificial sequence
366 <220> FEATURE:
367 <223> OTHER INFORMATION: VL backward primer for light chain variable region
368 of the PH1 Fab antibody with additional linker and
369 restriction sites
371 <400> SEQUENCE: 13
373 gccgatcgct ctggtcaccg tctcaagcgg aggcggtgca cttgaaattg tgctgactca    60
375 g                                                61
378 <210> SEQ ID NO: 14
379 <211> LENGTH: 50
380 <212> TYPE: DNA
381 <213> ORGANISM: artificial sequence
383 <220> FEATURE:
384 <223> OTHER INFORMATION: VL forward primer for light chain variable region
385 of PH1 Fab antibody with additional linker and
386 restriction sites
388 <400> SEQUENCE: 14

```

FYT.

Use of 'n' and/or 'Xaa' has been detected in the Sequence Listing. Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using 'n' or 'Xaa'.

VERIFICATION SUMMARY

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Input Set : A:\SEQ DYX-015.1.txt

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L:813 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:886 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
L:902 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34
L:918 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35
L:920 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35
L:936 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36
L:938 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36
L:954 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:1067 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45
L:1098 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47
L:1264 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:59
L:1323 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63